



(B)

Thu Jul 17 16:24:30 2001 [BLASTP 2.1.3 [Apr-1-2001], NCBI]
/home/.../va/Molbio/carpenda/templ/pl.DNA35639 (390 aa)

Sequences producing High-scoring Segment Pairs:

		Score	Match	Pct	E-val
1	P_AAB53082 ✓ Human angiogenesis-associated protein PRO	2012	390	100	0.0
2	P_AAB80219 ✓ Human PRO246 protein - Homo sapiens.	2012	390	100	0.0
3	P_AAB31207 ✓ human polypeptide PRO246 - Homo sapiens.	2012	390	100	0.0
4	P_AAB68599 ✓ PRO246 - Homo sapiens.	2012	390	100	0.0
5	P_AAB88358 ✓ Human membrane or secretory protein clone	2012	390	100	0.0
6	P_AAY94999 ✓ Human secreted protein vc51_1, SEQ ID NO:	2012	390	100	0.0
7	P_AAY88574 ✓ Human PRO246 amino acid sequence - Homo s	2012	390	100	0.0
8	P_AAY05286 ✓ EGF-like homologue PRO246 - Homo sapiens.	2012	390	100	0.0
9	P_AAY13351 ✓ protein PRO246 - Homo sapiens.	2012	390	100	0.0
10	P_AAY27096 ✓ Human viral receptor protein (ACVRP) - Ho	2012	390	100	0.0
11	P_AAB90818 ✓ Human shear stress-response protein SEQ I	2004	389	100	0.0
12	P_AAY76303 ✓ Fragment of human secreted protein encode	2003	388	100	0.0
13	P_AAB65832 Human INTERCEPT 258 SEQ ID NO: 28 - Homo	1734	341	94	0.0
14	P_AAB65906 Human secreted protein related protein SE	1732	340	94	0.0
15	P_AAB65907 Human secreted protein related protein SE	1730	340	94	0.0
16	P_AAB65905 Human secreted protein related protein SE	1730	340	94	0.0
17	P_AAB65904 Human secreted protein related protein SE	1730	340	94	0.0

>1 P_AAB53082 Human angiogenesis-associated protein PRO246, SEQ ID NO:96 - Homo sapiens. (390 aa) [1 seg]

Score = 2012 (779 bits), Expect = 0.0

Identities = 390/390 (100%), Positives = 390/390 (100%), at 1,1-390,390

```
DNA35639      1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV
*****
P_AAB53082      1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV
*****

DNA35639     61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD
*****
P_AAB53082     61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD
*****

DNA35639    121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLPAPPSCRLQGVPHVGANVTLSQCSPRSK
*****
P_AAB53082    121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLPAPPSCRLQGVPHVGANVTLSQCSPRSK
*****

DNA35639    181 PAVQYQWDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNTLE
*****
P_AAB53082    181 PAVQYQWDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNTLE
*****

DNA35639    241 VSTGPGAADVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS
*****
P_AAB53082    241 VSTGPGAADVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS
*****

DNA35639    301 SDTISKNGTLSSVTSARALRPPHGP RP GAL TPTPSLSSQALPSRLPTTDGAHPQPISP
*****
P_AAB53082    301 SDTISKNGTLSSVTSARALRPPHGP RP GAL TPTPSLSSQALPSRLPTTDGAHPQPISP
*****

DNA35639    361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV
*****
P_AAB53082    361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV
*****
```

>2 P_AAB80219 Human PRO246 protein - Homo sapiens. (390 aa) [1 seg]

BLAST RESULTS B-1

Score = 2012 (779 bits), Expect = 0.0
Identities = 390/390 (100%), Positives = 390/390 (100%), at 1,1-390,390

```
DNA35639      1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV
*****
P_AAB80219    1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

DNA35639     61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD
*****
P_AAB80219    61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD

DNA35639    121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSQCSPRSK
*****
P_AAB80219   121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSQCSPRSK

DNA35639    181 PAVQYQWDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE
*****
P_AAB80219   181 PAVQYQWDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE

DNA35639    241 VSTGPGAADVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS
*****
P_AAB80219   241 VSTGPGAADVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS

DNA35639    301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISP
*****
P_AAB80219   301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISP

DNA35639    361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV
*****
P_AAB80219   361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV
```

>3 P_AAB31207 human polypeptide PRO246 - Homo sapiens. (390 aa) [1 seg]
Score = 2012 (779 bits), Expect = 0.0
Identities = 390/390 (100%), Positives = 390/390 (100%), at 1,1-390,390

```
DNA35639      1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV
*****
P_AAB31207    1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

DNA35639     61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD
*****
P_AAB31207    61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD

DNA35639    121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSQCSPRSK
*****
P_AAB31207   121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSQCSPRSK

DNA35639    181 PAVQYQWDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE
*****
P_AAB31207   181 PAVQYQWDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE

DNA35639    241 VSTGPGAADVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS
*****
P_AAB31207   241 VSTGPGAADVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS

DNA35639    301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISP
*****
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BLAST RESULTS B-2

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P_AAB31207 301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISP
DNA35639 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV
*****
P_AAB31207 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

```

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>4 P_AAB68599 PRO246 - Homo sapiens. (390 aa) [1 seg]
Score = 2012 (779 bits), Expect = 0.0
Identities = 390/390 (100%), Positives = 390/390 (100%), at 1,1-390,390

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```

DNA35639 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV
*****
P_AAB68599 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV
DNA35639 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD
*****
P_AAB68599 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD
DNA35639 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNLVLPAPPSCRLQGVPVHGAVNTLSCQSPRSK
*****
P_AAB68599 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNLVLPAPPSCRLQGVPVHGAVNTLSCQSPRSK
DNA35639 181 PAVQYQWDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE
*****
P_AAB68599 181 PAVQYQWDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE
DNA35639 241 VSTGPGAADVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS
*****
P_AAB68599 241 VSTGPGAADVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS
DNA35639 301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISP
*****
P_AAB68599 301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISP
DNA35639 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV
*****
P_AAB68599 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

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>5 P_AAB88358 Human membrane or secretory protein clone PSEC0086 - Homo (390 aa)
[1 seg]
Score = 2012 (779 bits), Expect = 0.0
Identities = 390/390 (100%), Positives = 390/390 (100%), at 1,1-390,390

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```

DNA35639 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV
*****
P_AAB88358 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV
DNA35639 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD
*****
P_AAB88358 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD
DNA35639 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNLVLPAPPSCRLQGVPVHGAVNTLSCQSPRSK
*****
P_AAB88358 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNLVLPAPPSCRLQGVPVHGAVNTLSCQSPRSK
DNA35639 181 PAVQYQWDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE
*****

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BLAST RESULTS B-3

```

P_AAB88358 181 PAVQYQWDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE
DNA35639 241 VSTGPGAADVAGAVVGTTLVGLGGLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS
*****
P_AAB88358 241 VSTGPGAADVAGAVVGTTLVGLGGLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS
DNA35639 301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISP
*****
P_AAB88358 301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISP
DNA35639 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV
*****
P_AAB88358 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

```

>6 P_AAY94999 Human secreted protein vc51_1, SEQ ID NO:38 - Homo sapiens. (390 aa) [1 seg]

Score = 2012 (779 bits), Expect = 0.0

Identities = 390/390 (100%), Positives = 390/390 (100%), at 1,1-390,390

```

DNA35639 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV
*****
P_AAY94999 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV
DNA35639 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD
*****
P_AAY94999 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD
DNA35639 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNLVPPAPPSCRLQGVPVHGAVNTLSCQSPRSK
*****
P_AAY94999 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNLVPPAPPSCRLQGVPVHGAVNTLSCQSPRSK
DNA35639 181 PAVQYQWDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE
*****
P_AAY94999 181 PAVQYQWDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE
DNA35639 241 VSTGPGAADVAGAVVGTTLVGLGGLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS
*****
P_AAY94999 241 VSTGPGAADVAGAVVGTTLVGLGGLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS
DNA35639 301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISP
*****
P_AAY94999 301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISP
DNA35639 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV
*****
P_AAY94999 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

```

>7 P_AAY88574 Human PRO246 amino acid sequence - Homo sapiens. (390 aa) [1 seg]

Score = 2012 (779 bits), Expect = 0.0

Identities = 390/390 (100%), Positives = 390/390 (100%), at 1,1-390,390

```

DNA35639 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV
*****
P_AAY88574 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV
DNA35639 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD
*****

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BLAST RESULTS B-A

```

P_AAY88574    61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD
DNA35639    121 SGPYSCSVNVQDKQGKSRGHSIKTLELNLVPPAPPSCRLQGVPVHGAVNTLSCQSPRSK
*****
P_AAY88574    121 SGPYSCSVNVQDKQGKSRGHSIKTLELNLVPPAPPSCRLQGVPVHGAVNTLSCQSPRSK
DNA35639    181 PAVQYQWDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE
*****
P_AAY88574    181 PAVQYQWDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE
DNA35639    241 VSTGPGAADVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS
*****
P_AAY88574    241 VSTGPGAADVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS
DNA35639    301 SDTISKNGTLSSVTSARALRPPHGP RP GALTPTPSLSSQALPSPRLPTTDGAHPQPI SP
*****
P_AAY88574    301 SDTISKNGTLSSVTSARALRPPHGP RP GALTPTPSLSSQALPSPRLPTTDGAHPQPI SP
DNA35639    361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV
*****
P_AAY88574    361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

```

>8 P_AAY05286 EGF-like homologue PRO246 - Homo sapiens. (390 aa) [1 seg]
Score = 2012 (779 bits), Expect = 0.0
Identities = 390/390 (100%), Positives = 390/390 (100%), at 1,1-390,390

```

DNA35639      1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV
*****
P_AAY05286      1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV
DNA35639     61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD
*****
P_AAY05286     61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD
DNA35639    121 SGPYSCSVNVQDKQGKSRGHSIKTLELNLVPPAPPSCRLQGVPVHGAVNTLSCQSPRSK
*****
P_AAY05286    121 SGPYSCSVNVQDKQGKSRGHSIKTLELNLVPPAPPSCRLQGVPVHGAVNTLSCQSPRSK
DNA35639    181 PAVQYQWDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE
*****
P_AAY05286    181 PAVQYQWDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE
DNA35639    241 VSTGPGAADVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS
*****
P_AAY05286    241 VSTGPGAADVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS
DNA35639    301 SDTISKNGTLSSVTSARALRPPHGP RP GALTPTPSLSSQALPSPRLPTTDGAHPQPI SP
*****
P_AAY05286    301 SDTISKNGTLSSVTSARALRPPHGP RP GALTPTPSLSSQALPSPRLPTTDGAHPQPI SP
DNA35639    361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV
*****
P_AAY05286    361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

```

>9 P_AAY13351 protein PRO246 - Homo sapiens. (390 aa) [1 seg]
Score = 2012 (779 bits), Expect = 0.0
Identities = 390/390 (100%), Positives = 390/390 (100%), at 1,1-390,390

BLAST RESULTS B-5

```

DNA35639      1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV
*****
P_AAY13351    1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

DNA35639     61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD
*****
P_AAY13351    61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD

DNA35639    121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSQCSPRSK
*****
P_AAY13351   121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSQCSPRSK

DNA35639    181 PAVQYQWDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE
*****
P_AAY13351   181 PAVQYQWDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE

DNA35639    241 VSTGPGAADVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS
*****
P_AAY13351   241 VSTGPGAADVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS

DNA35639    301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISP
*****
P_AAY13351   301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISP

DNA35639    361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV
*****
P_AAY13351   361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

```

>10 P_AAY27096 Human viral receptor protein (ACVRP) - Homo sapiens. (390 aa) [1 seg]

Score = 2012 (779 bits), Expect = 0.0

Identities = 390/390 (100%), Positives = 390/390 (100%), at 1,1-390,390

```

DNA35639      1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV
*****
P_AAY27096    1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

DNA35639     61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD
*****
P_AAY27096    61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD

DNA35639    121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSQCSPRSK
*****
P_AAY27096   121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSQCSPRSK

DNA35639    181 PAVQYQWDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE
*****
P_AAY27096   181 PAVQYQWDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE

DNA35639    241 VSTGPGAADVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS
*****
P_AAY27096   241 VSTGPGAADVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS

DNA35639    301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISP
*****
P_AAY27096   301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISP

```

BLAST RESULTS B-7

```
DNA35639 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV
*****
P_AAY27096 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

>11 P_AAB90818 Human shear stress-response protein SEQ ID NO: 144 - Homo (390
aa) [1 seg]
Score = 2004 (776 bits), Expect = 0.0
Identities = 389/390 (99%), Positives = 389/390 (99%), at 1,1-390,390

DNA35639 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV
*****
P_AAB90818 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

DNA35639 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD
*****
P_AAB90818 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD

DNA35639 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPVHGAVNTLSCQSPRSK
*****
P_AAB90818 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPVHGAVNTLSCQSPRSK

DNA35639 181 PAVQYQWDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE
*****
P_AAB90818 181 PAVQYQWDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE

DNA35639 241 VSTGPGAADVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS
*****
P_AAB90818 241 VSTGPGAADVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS

DNA35639 301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSRLPTTDGAHPQPISP
*****
P_AAB90818 301 SDTISKNGTLSSVTSARALWPPHGPPRPGALTPTPSLSSQALPSRLPTTDGAHPQPISP

DNA35639 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV
*****
P_AAB90818 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

>12 P_AAY76303 Fragment of human secreted protein encoded by gene 29 - Homo (389
aa) [1 seg]
Score = 2003 (776 bits), Expect = 0.0
Identities = 388/389 (99%), Positives = 389/389 (99%), at 1,1-389,389

DNA35639 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV
*****
P_AAY76303 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

DNA35639 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD
*****
P_AAY76303 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD

DNA35639 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPVHGAVNTLSCQSPRSK
*****
P_AAY76303 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPVHGAVNTLSCQSPRSK

DNA35639 181 PAVQYQWDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE
*****
```

BLAST RESULTS B-B

P_AAY76303 181 PAVQYQWDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNTLE
DNA35639 241 VSTGPGAADVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS

P_AAY76303 241 VSTGPGAADVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS
DNA35639 301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISP

P_AAY76303 301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISP
DNA35639 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSL

P_AAY76303 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSL

>13 P_AAB65832 Human INTERCEPT 258 SEQ ID NO: 28 - Homo sapiens. (370 aa) [1 seg]
Score = 1734 (672 bits), Expect = 0.0
Identities = 341/362 (94%), Positives = 344/362 (94%), Gaps = 7/362 (1%), at 1,1-355,362

DNA35639 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV
***** **
P_AAB65832 1 MISLPGPLVTNLXRFLFLGLSALAPPSRAQLQLHLPANRLQAVEEGESGASAWYTLHREV
DNA35639 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD

P_AAB65832 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRVEGLQEKD
DNA35639 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLPAPPSCRLQGVPVHGAVNTLSCQSPRSK

P_AAB65832 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLPAPPSCRLQGVPVHGAVNTLSCQSPRSK
DNA35639 181 PAVQYQWDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNTLE

P_AAB65832 181 PAVQYQWDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNTLE
DNA35639 241 VSTGPGAADVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS

P_AAB65832 241 VSTGPGAADVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS
DNA35639 301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPR-----LPTTDGA

P_AAB65832 301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRHAHDRWGPPSTNIP
DNA35639 354 HP
**
P_AAB65832 361 HP

>14 P_AAB65906 Human secreted protein related protein SEQ ID NO: 138 - Homo (370 aa) [1 seg]
Score = 1732 (671 bits), Expect = 0.0
Identities = 340/362 (93%), Positives = 344/362 (94%), Gaps = 7/362 (1%), at 1,1-355,362

DNA35639 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV
***** **
P_AAB65906 1 MISLPGPLVTNLXRFLFLGLSALAPPSRAQLQLHLPANRLQAVEEGESGASAWYTLHREV

DNA35639	61	SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD *****
P_AAB65906	61	SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRVEGLQEKD
DNA35639	121	SGPYSCSVNVQDKQGKSRGHSIKTLELNLVPPAPPSCRLQGVPVHGAVNTLSCQSPRSK *****
P_AAB65906	121	SGPYSCSVNVQDKQGKSRGHSIKTLELNLVPPAPPSCRIQGVPVHGAVNTLSCQSPRSK
DNA35639	181	PAVQYQWDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNTLE *****
P_AAB65906	181	PAVQYQWDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNTLE
DNA35639	241	VSTGPGAADVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS *****
P_AAB65906	241	VSTGPGAADVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS
DNA35639	301	SDTISKNGTLSSVTSARALRPPHGP RP GALTPTPSLSSQALPSPR-----LPTTDGA ***** *.*
P_AAB65906	301	SDTISKNGTLSSVTSARALRPPHGP RP GALTPTPSLSSQALPSPRHAHDRWGPPSTNIP
DNA35639	354	HP **
P_AAB65906	361	HP

>15 P_AAB65907 Human secreted protein related protein SEQ ID NO: 140 - Homo (370 aa) [1 seg]
Score = 1730 (671 bits), Expect = 0.0
Identities = 340/362 (93%), Positives = 343/362 (93%), Gaps = 7/362 (1%), at 1,1-355,362

DNA35639	1	MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV ***** **
P_AAB65907	1	MISLPGPLVTNLXRFLFLGLSALAPPSRAQLQLHLPANRLQAVEEGESGASAWYTLHREV
DNA35639	61	SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD *****
P_AAB65907	61	SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRVEGLQEKD
DNA35639	121	SGPYSCSVNVQDKQGKSRGHSIKTLELNLVPPAPPSCRLQGVPVHGAVNTLSCQSPRSK *****
P_AAB65907	121	SGPYSCSVNVQDKQGKSRGHSIKTLELNLVPPAPPSCRLQGVPVHGAVNTLSCQSPRSK
DNA35639	181	PAVQYQWDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNTLE * *****
P_AAB65907	181	PVVQYQWDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNTLE
DNA35639	241	VSTGPGAADVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS *****
P_AAB65907	241	VSTGPGAADVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS
DNA35639	301	SDTISKNGTLSSVTSARALRPPHGP RP GALTPTPSLSSQALPSPR-----LPTTDGA ***** *.*
P_AAB65907	301	SDTISKNGTLSSVTSARALRPPHGP RP GALTPTPSLSSQALPSPRHAHDRWGPPSTNIP
DNA35639	354	HP **

BLAST RESULTS B-9

P_AAB65907 361 HP

>16 P_AAB65905 Human secreted protein related protein SEQ ID NO: 136 - Homo (370 aa) [1 seg]
Score = 1730 (671 bits), Expect = 0.0
Identities = 340/362 (93%), Positives = 343/362 (93%), Gaps = 7/362 (1%), at 1,1-355,362

```
DNA35639      1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV
*****
P_AAB65905      1 MISLPGPLVTNLXRFLFLGLSALAPPSRAQLQLHLPANRLQAVEEGESGASAWYTLHREV

DNA35639      61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD
*****
P_AAB65905      61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLAYSMPSRNLSLRVEGLQEKD

DNA35639     121 SGPYSCSVNVQDKQGKSRGHSIKTLELNLVPPAPPSCRLQGVPVHGANGVTLSQCSPRSK
*****
P_AAB65905     121 SGPYSCSVNVQDKQGKSRGHSIKTLELNLVPPAPPSCRLQGVPVHGANGVTLSQCSPRSK

DNA35639     181 PAVQYQWDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE
*****
P_AAB65905     181 PAVQYQWDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE

DNA35639     241 VSTGPGAADVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS
*****
P_AAB65905     241 VSTGPGAADVAAEAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS

DNA35639     301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPR-----LPTTDGA
*****
P_AAB65905     301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRHAHDRWGPPSTNIP

DNA35639     354 HP
**
P_AAB65905     361 HP
```

>17 P_AAB65904 Human secreted protein related protein SEQ ID NO: 134 - Homo (370 aa) [1 seg]
Score = 1730 (671 bits), Expect = 0.0
Identities = 340/362 (93%), Positives = 343/362 (93%), Gaps = 7/362 (1%), at 1,1-355,362

```
DNA35639      1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV
*****
P_AAB65904      1 MISLPGPLVTNLXRFLFLGLSALAPPSRAQLQLHLPANRLQAVEEGESGASAWYTLHREA

DNA35639      61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD
*****
P_AAB65904      61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRVEGLQEKD

DNA35639     121 SGPYSCSVNVQDKQGKSRGHSIKTLELNLVPPAPPSCRLQGVPVHGANGVTLSQCSPRSK
*****
P_AAB65904     121 SGPYSCSVNVQDKQGKSRGHSIKTLELNLVPPAPPSCRLQGVPVHGANGVTLSQCSPRSK

DNA35639     181 PAVQYQWDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE
*****
P_AAB65904     181 PAVQYQWDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE
```

BLAST RESULTS B-10

DNA35639	241	VSTGPGAADVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWKS

P_AAB65904	241	VSTGPGAADVAEAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWKS
DNA35639	301	SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPR-----LPTTDGA

P_AAB65904	301	SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRHAHDRWGPPSTNIIP
DNA35639	354	HP
		**
P_AAB65904	361	HP

Blast Results B-11